



ModifiedSequenceListing.txt
SEQUENCE LISTING

<110> Wageningen Centre for Food Sciences

<120> Novel mannose-specific adhesins and their use

<130> P212925EP

<140> 10/594,258

<141> 2006-09-25

<150> EP04075945.8

<151> 2004-03-23

<160> 16

<170> PatentIn version 3.1

<210> 1

<211> 1010

<212> PRT

<213> Lactobacillus plantarum

<400> 1

Met Leu Lys Lys Asp Asn Phe Gly Glu His Lys Thr His Tyr Lys Leu
1 5 10 15

Tyr Lys Cys Gly Lys Asn Trp Ala Ile Met Gly Ile Thr Leu Val Ser
20 25 30

Leu Gly Val Gly Thr Val Thr Met Thr Arg Ala Ala Ala Asp Ser
35 40 45

Glu Val Thr Asn Asp Ser Ala Ser Gln His Val Thr Ser Ile Ser Thr
50 55 60

Asp Ala Ser Lys Asn Gln His Thr Ser Ser Asn Val Ile Leu Thr Asn
65 70 75 80

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Asp Asp Lys Ser Val Ser Ala Ser Ile Asn Gln Asp Ala Ser Ala Ser
 85 90 95
 Val Val Asn Lys Ala Val Ser Ala Thr Ser Gln Glu Asn Ser Ser Val
 100 105 110
 Gln Asn Thr Ser Gln Ala Thr Ser Thr Ser Lys Gln Glu Ser Ser Ser
 115 120 125
 Thr Lys Asn Thr Ser Gln Thr Thr Ser Thr Ser Asn Gln Glu Ala Asn
 130 135 140
 Ser Ala Lys Ser Ile Asn Gln Thr Thr Arg Thr Ser Lys Gln Glu Ser
 145 150 155 160
 Ser Ser Thr Lys Asn Thr Ser Gln Thr Thr Ser Thr Ser Asn Gln Glu
 165 170 175
 Ala Asn Ser Ala Lys Ser Ile Asn Gln Thr Thr Arg Thr Ser Asn Gln
 180 185 190
 Glu Ser Ser Ser Ala Lys Asn Thr Ser Gln Thr Thr Ser Thr Ser Ser
 195 200 205
 Arg Lys Ile Asn Ser Thr Lys Ser Gln Ala Gln Ser Leu Thr Ile Thr
 210 215 220
 Thr Thr Gly Lys Ala Val Arg Ala Thr Ser Thr Ser Val Lys Lys Tyr
 225 230 235 240
 Ser Thr Lys Thr Lys Val Ser Tyr Ser Thr Leu Leu Gln Gln Leu Arg
 245 250 255
 Thr Ser Lys Ala Leu Ile Ser Asp Glu Ala Ala Leu Thr His Val Asp
 260 265 270
 Lys Asp Asn Phe Leu Lys Tyr Phe Ser Leu Asn Gly Ser Ala Thr Tyr
 275 280 285
 Asp Ala Lys Thr Gly Ile Val Thr Ile Thr Pro Asn Gln Asn Asn Gln
 290 295 300
 Val Gly Asn Phe Ser Leu Thr Ser Lys Ile Asp Met Asn Lys Ser Phe
 305 310 315 320
 Thr Leu Thr Gly Gln Val Asn Leu Gly Ser Asn Pro Asn Gly Ala Asp
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325

330

335

Gly Ile Gly Phe Ala Phe His Ser Gly Asn Thr Thr Asp Val Gly Asn
 340 345 350

Ala Gly Gly Asn Leu Gly Ile Gly Gly Leu Gln Asp Ala Ile Gly Phe
 355 360 365

Lys Leu Asp Thr Trp Phe Asn Ser Tyr Gln Ala Pro Ser Ser Asp Lys
 370 375 380

Asn Gly Ser Glu Ile Ser Ser Thr Asn Ser Asn Gly Phe Gly Trp Asn
 385 390 395 400

Gly Asp Ser Ala Asn Ala Pro Tyr Gly Thr Phe Val Lys Thr Ser Asn
 405 410 415

Gln Glu Ile Ser Thr Ala Asn Gly Ser Lys Val Gln Arg Trp Trp Ala
 420 425 430

Gln Asp Thr Gly Glu Ser Gln Ala Leu Ser Lys Ala Asp Ile Asp Gly
 435 440 445

Asn Phe His Asp Phe Val Val Asn Tyr Asp Gly Ala Thr Arg Thr Leu
 450 455 460

Thr Val Ser Tyr Thr Gln Ala Ser Gly Lys Val Leu Thr Trp Lys Thr
 465 470 475 480

Thr Val Asp Ser Ser Tyr Gln Ala Met Ala Met Val Val Ser Ala Ser
 485 490 495

Thr Gly Ala Ala Lys Asn Leu Gln Gln Phe Lys Leu Thr Ser Phe Asp
 500 505 510

Phe Gln Glu Ala Ala Thr Val Asn Val Lys Tyr Val Asp Thr Thr Gly
 515 520 525

His Gln Leu Ala Gln Gly Thr Ala Asn Tyr Pro Asp Gly Ala Tyr Val
 530 535 540

Asn Gly Arg Tyr Thr Thr Lys Gln Leu Ile Ile Pro Asn Tyr Arg Phe
 545 550 555 560

Ile Lys Met Asp Asp Gly Ser Val Thr Gly Thr Lys Ser Leu Asp Ala
 565 570 575

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Asn Gly Thr Leu Ile Gln Ser Gly Asp Asn Gly Thr Val Ile Tyr Val
580 585 590

Tyr Val Pro Glu Tyr Met Ala Ile Val Lys Thr Val Asn Glu Thr Ile
595 600 605

Asn Tyr Val Asp Glu Asn Gly His Ala Leu Thr Thr Ser Tyr Thr Ala
610 615 620

Asn Pro Ile His Ile Leu Thr Val Thr Asn Pro Val Asp Gly Thr Thr
625 630 635 640

Thr Thr Tyr Tyr Ser Thr Ile Thr Thr Ser Ile Glu Leu Asp Ala Thr
645 650 655

Thr Gly Arg Pro Val Asp Ser Gly Trp Val Leu Gly Asn Ser Gln Asp
660 665 670

Phe Asp Ala Val Thr Asn Pro Gln Ile Lys Gly Tyr Thr Val Thr Ser
675 680 685

Thr Asp Ala Pro Asn Ser Asp Leu Gln His Val Ser Ala Gln Thr Val
690 695 700

Thr Gly Asp Ser Gly Asp Leu Glu Phe Thr Val Val Tyr Thr Lys Asn
705 710 715 720

Ala Pro Ile Val Thr Thr Glu Ser Lys Thr Val Asn Glu Thr Ile His
725 730 735

Tyr Val Tyr Thr Asp Gly Thr Thr Ala His Asp Asp Tyr Val Ala Gln
740 745 750

Pro Ile Thr Phe Thr Arg Thr Val Phe Thr Asp Ala Val Thr Gly Glu
755 760 765

Lys Thr Tyr Gly Gly Trp Ser Ala Ala Gln Gln Phe Ala Ala Val Asp
770 775 780

Ser Pro Ala Ile Lys Gly Tyr Thr Pro Asp Gln Ser Lys Ile Ser Thr
785 790 795 800

Gln Thr Val Thr Gly Asp Ser Ser Asp Leu Glu Phe Thr Ile Val Tyr
805 810 815

Thr Lys Asn Ala Pro Thr Val Thr Thr Glu Ser Lys Thr Val Asn Glu
820 825 830

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Thr Ile His Tyr Val Tyr Thr Asp Gly Thr Ile Ala His Asp Asp Tyr
835 840 845

Val Ala Gln Pro Ile Thr Phe Thr Arg Thr Val Ser Thr Asp Ala Val
850 855 860

Thr Gly Glu Lys Thr Tyr Gly Gly Trp Ser Ala Ala Gln Gln Phe Ala
865 870 875 880

Ala Val Asp Ser Pro Ala Ile Lys Gly Tyr Thr Pro Asp Gln Ser Lys
885 890 895

Ile Ser Thr Gln Thr Val Thr Gly Asp Ser Ser Asp Leu Glu Phe Thr
900 905 910

Val Val Tyr Lys Ala Asp Ser Thr Ser Thr Lys Pro Val Lys Pro Glu
915 920 925

Gln Pro Thr Ile Pro Thr Thr Pro Thr Glu Pro Val Lys Pro Gly Gln
930 935 940

Leu Thr Thr Pro Ala Lys Pro Asp Gln Pro Met Thr Ser Asp Lys Ser
945 950 955 960

Val Gln Thr Ile Thr Ile Lys Phe Val Gly Gln Arg Leu Pro Gln Thr
965 970 975

Asn Glu Thr Asp Gln Gln His Met Thr Leu Ser Gly Leu Leu Leu Leu
980 985 990

Ala Met Ser Gly Leu Leu Gly Leu Leu Gly Met Ala Lys Arg Gln His
995 1000 1005

Lys Glu
1010

<210> 2

<211> 3030

<212> DNA

<213> Lactobacillus plantarum

<400> 2

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aaaaactggg ctattatggg gattacgttg gtttcattgg gggtaggtac tgttactatg 120

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gatgataaaa	gtgttagtgc	atcaattaat	caagacgcta	gcgcgagtgt	tgtcaataag	300
gcggtcagcg	caactagcca	agaaaatagt	agcgttcaaa	atactagtca	ggcaaccagt	360
acaagcaaac	aagaatccag	tagtacgaaa	aatactagtc	agacaaccag	tacaagcaat	420
caagaagcta	acagtgccaa	gagtattaat	caaacgaccc	gtacaagcaa	acaagaatcc	480
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ttaacaatta	cgactacggg	caaagcgggt	cgtgctacct	cgactagtgt	taaaaagtac	720
tccaccaaga	caaaagtgtc	atatagcaca	ttgttacagc	agcttcgtac	aagtaaagcg	780
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agtttgaacg	gatctgcaac	atatgatgcc	aagacgggaa	ttgtaactat	tacgccaat	900
caaaataatc	aagttggtaa	tttttcatta	accagtaaga	ttgatatgaa	taaaagcttt	960
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agctacaccg	ccaatcccat	ccatatattg	accgtgacga	atccggtgga	tggaacgacg	1920
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<211> 234

<212> PRT

<213> Lactobacillus plantarum

<400> 3

Met Lys Ser Lys Gln His Pro Gly Leu Lys Trp Leu Gly Arg Gly Val
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Phe Val Leu Leu Val Leu Val Ser Leu Ala Leu Ile Phe Asn Glu Gln
20 25 30

Ile Lys Ser Trp Leu Val Ser Ser Tyr Ser Pro Thr Val Thr Ala Lys
35 40 45

Thr Val Lys Gln Asn Thr Lys Lys Lys Ser Asp Phe Asn Phe Ser Lys
50 55 60

ModifiedSequenceListing.txt

Val Lys Ser Leu Asp Phe Gln Thr Val Ala Lys Ala Arg Met Asn Lys
65 70 75 80

Asn Ala Ile Asn Val Ile Gly Ser Ile Ala Ile Pro Ser Val Asp Leu
85 90 95

Tyr Leu Pro Ile Gly Asn Gly Val Ser Asn Glu Thr Leu Ala Leu Ala
100 105 110

Ala Gly Thr Met Lys Ala Asn Gln Lys Met Gly Gln Gly Asn Tyr Ala
115 120 125

Leu Ala Gly His His Met Ile Lys His Gly Ala Leu Phe Ser Pro Leu
130 135 140

Tyr Tyr Lys Ser Lys Val Gly Gln Met Ile Tyr Val Ser Asp Ala Lys
145 150 155 160

Lys Ile Tyr Ala Tyr Lys Thr Ser Gln Arg Thr Phe Ile Lys Ala Thr
165 170 175

Asp Val Gln Val Ile Asp Asp Val Pro Gly Gln Lys Leu Ile Thr Leu
180 185 190

Ile Thr Cys Asp Lys Thr Gly Ala Gly Arg Leu Met Ile Arg Gly Lys
195 200 205

Tyr Glu Gln Gln Trp Ser Phe Lys Ser Ala Pro Thr Gln Val Gln Lys
210 215 220

Ala Phe Thr Ser His Phe Asn Asn Lys Tyr
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<210> 4

<211> 702

<212> DNA

<213> Lactobacillus plantarum

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tactcgccga ccgttacggc taagacgggtt aagcagaata cgaagaagaa gagcgatttt 180

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ggtcgcttaa tgattcgcg taagtacgaa cagcaatggc cgtttaagtc ggcgccaact		660
caggttcaga aggcctttac aagtcatttt aataacaaat at		702

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<212> DNA

<213> Artificial

<220>

<221> misc_feature

<223> oligonucleotide

<400> 5

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<210> 6

<211> 20

<212> DNA

<213> Artificial

<220>

<221> misc_feature

<223> oligonucleotide

<400> 6

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<211> 32

<212> DNA

<213> Artificial

<220>

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<223> oligonucleotide

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<223> oligonucleotide

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cgtgtttcctt ggaagacttc

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<210> 9

<211> 20

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<213> Artificial

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<210> 11

<211> 32

<212> DNA

<213> Artificial

<220>

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<223> oligonucleotide

<400> 11

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<223> oligonucleotide

ModifiedSequenceListing.txt

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<210> 13

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<223> oligonucleotide

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ModifiedSequenceListing.txt

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<223> oligonucleotide

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